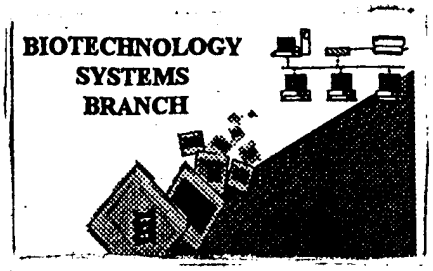
0590
0606



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/084,380
Source: OIPE
Date Processed by STIC: 6/5/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom!
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or ther delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/084,380

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ✓	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,380

DATE: 06/05/2002
TIME: 10:30:11

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\06052002\J084380.raw

pp 1-4
Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: CHAIN, Daniel G.
W--> 5 <120> TITLE OF INVENTION: RECOMBINANT ANTIBODIES SPECIFIC FOR BETA-AMYLOID ENDS, DNA
W--> 6 ENCODING AND METHODS OF USE THEREOF
W--> 7 <130> FILE REFERENCE: CHAIN1B
W--> 8 <140> CURRENT APPLICATION NUMBER: 10/084,380
C--> 9 <141> CURRENT FILING DATE: 2002-02-28
10 <150> PRIOR APPLICATION NUMBER: PCT/US98/06900
11 <151> PRIOR FILING DATE: 1997-04-09
E--> 12 <160> NUMBER OF SEQ ID: 8 18 shown (duplicated sequences starting on p. 3
13 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

W--> 14 <210> SEQ ID NO: 1
15 <211> LENGTH: 59
16 <212> TYPE: PRT
17 <213> ORGANISM: Homo sapiens
W--> 18 <400> SEQUENCE: 1
19 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
E--> 20 1 5 ~~5~~ 10 15 ~~10~~
E--> 21 ~~15~~
22 His His Gln Lys Leu Val Phe Phe ~~Ala Glu Asp Val Gly Ser Asn~~ Lys
E--> 23 ~~20~~ 25
E--> 24 ~~30~~
25 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val ~~Ile~~ Ala Thr Val
E--> 26 35 40 45
27 Ile Val Ile Thr Leu Val ~~Met Leu Lys Lys Lys~~
E--> 28 ~~50 50~~ "50" is duplicated - do you mean "55?"
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 6
31 <212> TYPE: PRT
32 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE WITH ARTIFICIAL
37 TERMINAL CYSTEINE RESIDUE
39 <400> SEQUENCE: 2
40 Asp Ala Glu Phe Arg Cys
E--> 41 1 5 misaligned number
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 8
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence

misaligned amino acid numbers (see item 3 on Error Summary Sheet)

RAW SEQUENCE LISTING DATE: 06/05/2002
PATENT APPLICATION: **US/10/084,380** TIME: 10:30:11

Input Set : **A:\PTO.PG.txt**
Output Set: **N:\CRF3\06052002\J084380.raw**

48 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE WITH ARTIFICIAL
50 TERMINAL CYSTEINE RESIDUE
52 <400> SEQUENCE: 3
53 Asp Ala Glu Phe Arg His Asp Cys
E--> 54 1 5 misaligned
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 8
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial sequence: HUMAN PEPTIDE WITH ARTIFICIAL
63 TERMINAL CYSTEINE RESIDUE
65 <400> SEQUENCE: 4
66 Cys Leu Met Val Gly Gly Val Val
E--> 67 1 5 misaligned
69 <210> SEQ ID NO: 5
70 <211> LENGTH: 8
71 <212> TYPE: PRT
72 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Description of Artificial sequence: HUMAN PEPTIDE WITH ARTIFICIAL
77 TERMINAL CYSTEINE RESIDUE
79 <400> SEQUENCE: 5
80 Cys Val Gly Gly Val Val Ile Ala
E--> 81 1 5 misaligned
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 6
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 6
89 Asp Ala Glu Phe Arg His
E--> 90 1 5 same
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 13
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 7
98 Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His
E--> 99 1 5 10
101 <210> SEQ ID NO: 8
102 <211> LENGTH: 4
103 <212> TYPE: PRT
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 8
107 Glu Phe Arg His
E--> 108 1 misaligned
111 <210> SEQ ID NO: 9
112 <211> LENGTH: 6

RAW SEQUENCE LISTING DATE: 06/05/2002
PATENT APPLICATION: US/10/084,380 TIME: 10:30:11

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\06052002\J084380.raw

113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence delete
W--> 115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 117 <400> SEQUENCE: 9
119 Glu Val His His Gln Cys
E--> 120 1 5
122 <210> SEQ ID NO: 10
123 <211> LENGTH: 12
124 <212> TYPE: PRT
125 <213> ORGANISM: Artificial Sequence
W--> 126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 128 <400> SEQUENCE: 10
130 Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
E--> 131 1 5 10
133 <210> SEQ ID NO: 11
134 <211> LENGTH: 8
135 <212> TYPE: PRT
136 <213> ORGANISM: Artificial Sequence
W--> 137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 139 <400> SEQUENCE: 11 dashes not permitted
E--> 141 Cys-Gly-Gly-Val-Val-Ile-Ala-Thr
E--> 142 1 5 ← insert — do not use TAB codes between numbers
146 <210> SEQ ID NO: 12
147 <211> LENGTH: 14 13 shown
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial Sequence
W--> 150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 152 <400> SEQUENCE: 12
E--> 154 Asn-Lys-Gly-Ala-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val delete dashes
E--> 155 1 5 10 ← insert numbers
157 <210> SEQ ID NO: 13
158 <211> LENGTH: 14
159 <212> TYPE: PRT
160 <213> ORGANISM: Artificial Sequence
W--> 161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
E--> 163 <400> SEQUENCE: 13 ← insert
E--> 165 Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr delete dashes
E--> 166 1 5 10 misaligned
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 6
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence why is Sequence 9 duplicated?
W--> 172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE

RAW SEQUENCE LISTING DATE: 06/05/2002
PATENT APPLICATION: US/10/084,380 TIME: 10:30:11

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\06052002\J084380.raw

W--> 174 <400> SEQUENCE: 9
176 Glu Val His His Gln Cys
E--> 177 1 5
181 <210> SEQ ID NO: 10
182 <211> LENGTH: 12
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence>
W--> 185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 187 <400> SEQUENCE: 10
189 Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
E--> 190 1 5 10
192 <210> SEQ ID NO: 11
193 <211> LENGTH: 8
194 <212> TYPE: PRT
195 <213> ORGANISM: Artificial Sequence>
W--> 196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 198 <400> SEQUENCE: 11
E--> 200 Cys-Gly-Gly-Val-Val-Ile-Ala-Thr
E--> 201 1 5
203 <210> SEQ ID NO: 12
204 <211> LENGTH: 14
205 <212> TYPE: PRT
206 <213> ORGANISM: Artificial Sequence>
W--> 207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
W--> 209 <400> SEQUENCE: 12
E--> 211 Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val
E--> 212 1 5 10
216 <210> SEQ ID NO: 13
217 <211> LENGTH: 14
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence>
W--> 220 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence: HUMAN PEPTIDE
E--> 222 <400> SEQUENCE: 12
E--> 224 Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr
E--> 225 1 5 10

?

why is Sequence 10 duplicated?

duplicated sequence

This is a duplicate of Seq. 12 except for extra Ile at location 6

duplicated sequence

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/05/2002
PATENT APPLICATION: US/10/084,380 TIME: 10:30:12

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\06052002\J084380.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 20,23

VERIFICATION SUMMARY DATE: 06/05/2002
PATENT APPLICATION: **US/10/084,380** TIME: 10:30:12

Input Set : **A:\PTO.PG.txt**
Output Set: **N:\CRF3\06052002\J084380.raw**

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12 M:283 W: Missing Blank Line separator, <160> field identifier
L:14 M:283 W: Missing Blank Line separator, <210> field identifier
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:20 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:41 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:54 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:67 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:81 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:90 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:108 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:115 M:283 W: Missing Blank Line separator, <220> field identifier
L:117 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:131 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:137 M:283 W: Missing Blank Line separator, <220> field identifier
L:139 M:283 W: Missing Blank Line separator, <400> field identifier
L:141 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:142 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:142 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:1 SEQ:11
L:150 M:283 W: Missing Blank Line separator, <220> field identifier
L:152 M:283 W: Missing Blank Line separator, <400> field identifier
L:154 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:155 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:155 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:1 SEQ:12
L:161 M:283 W: Missing Blank Line separator, <220> field identifier
L:163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:12
L:163 M:283 W: Missing Blank Line separator, <400> field identifier
L:165 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:166 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:1 SEQ:13
L:172 M:283 W: Missing Blank Line separator, <220> field identifier
L:174 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:185 M:283 W: Missing Blank Line separator, <220> field identifier
L:187 M:283 W: Missing Blank Line separator, <400> field identifier
L:190 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:196 M:283 W: Missing Blank Line separator, <220> field identifier
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:200 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11